

AP20 Rec'd PCT/PTO 14 JUL 2006

<110> Korea Research Institute of Bioscience and Biotechnology
 <120> Rapid screening method of translational fusion partners for
 producing recombinant proteins and translational fusion partners
 screened therefrom

<150> KR10-2004-0003957

<151> 2004-01-19

<160> 45

<170> Kopatentin 1.71

<210> 1

<211> 105

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> PEPTIDE

<222> (1)..(105)

<223> TFP1

<400> 1
 Met Phe Asn Arg Phe Asn Lys Phe Gln Ala Ala Val Ala Leu Ala Leu
 1 5 10 15

Leu Ser Arg Gly Ala Leu Gly Asp Ser Tyr Thr Asn Ser Thr Ser Ser
 20 25 30

Ala Asp Leu Ser Ser Ile Thr Ser Val Ser Ser Ala Ser Ala Ser Ala
 35 40 45

Thr Ala Ser Asp Ser Leu Ser Ser Ser Asp Gly Thr Val Tyr Leu Pro
 50 55 60

Ser Thr Thr Ile Ser Gly Asp Leu Thr Val Thr Gly Lys Val Ile Ala
 65 70 75 80

Thr Glu Ala Val Glu Val Ala Ala Gly Gly Lys Leu Thr Leu Leu Asp
 85 90 95

Gly Glu Lys Tyr Val Phe Ser Ser Asp
 100 105

<210> 2

<211> 430

<212> DNA

<213> Saccharomyces cerevisiae

<220>

<221> gene

<222> (1)..(430)

<223> TFP1

<400> 2
 gatcgatcata ttactcttg ttctcataat agcagtcctaa gttttcatct ttgcaagctt 60
 tactatttct ttctttttat tggtaaactc tcgcccatta caaaaaaaaa agagatgttc 120
 aatcgtttta acaaattcca agctgctgtc gctttggccc tactctctcg cggcgctctc 180
 ggtgactctt acaccaatag caccctctcc gcagacttga gtctatcac ttccgtctcg 240
 tcagctagtg caagtggccac cgcttcggac tcactttctt ccagtgacgg taccgtttat 300
 ttgccatcca caacaattag cggtgatctc acagttactg gtaaagtaat tgcaaccgag 360
 gccgtggaag tcgctgcccg tggtaagttg actttacttg acggtgaaaa atacgtcttc 420
 tcatctgac 430

<210> 3

<211> 117

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<212> PRT
 <213> *Saccharomyces cerevisiae*

<220>
 <221> PEPTIDE
 <222> (1)..(117)
 <223> TFP2

<400> 3
 Met Thr Pro Tyr Ala Val Ala Ile Thr Val Ala Leu Leu Ile Val Thr
 1 5 10 15
 Val Ser Ala Leu Gln Val Asn Asn Ser Cys Val Ala Phe Pro Pro Ser
 20 25 30
 Asn Leu Arg Gly Lys Asn Gly Asp Gly Thr Asn Glu Gln Tyr Ala Thr
 35 40 45
 Ala Leu Leu Ser Ile Pro Trp Asn Gly Pro Pro Glu Ser Leu Arg Asp
 50 55 60
 Ile Asn Leu Ile Glu Leu Glu Pro Gln Val Ala Leu Tyr Leu Leu Glu
 65 70 75 80
 Asn Tyr Ile Asn His Tyr Tyr Asn Thr Thr Arg Asp Asn Lys Cys Pro
 85 90 95
 Asn Asn His Tyr Leu Met Gly Gly Gln Leu Gly Ser Ser Ser Asp Asn
 100 105 110
 Arg Ser Leu Asn Asp
 115

<210> 4
 <211> 424
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> gene
 <222> (1)..(424)
 <223> TFP2

<400> 4
 gatctcattg gattcaagag aaagaaactc tatactggcg ccaaattagc agtgtcaaat 60
 ttcgaaaagg tgaatgacgc ctatgcagta gcaattaccg tggccitact aattgtaaca 120
 gtgagcgcac tccaggtaaa caattcatgt gtcgcttttc cgccatcaaa tctcagagga 180
 aaaaatggag acggtactaa tgaacagtat gcaactgcac tactttctat tccctggaat 240
 ggacctccig agtcattgag ggatattaat cttattgaac tcgaaccgca agttgcactc 300
 tatttgctcg aaaattatat taaccattac tacaacacca caagagacaa taagtgcctt 360
 aataaccact acctaatggg agggcagttg ggtagctcat cggataatag gagtttgaac 420
 gatc 424

<210> 5
 <211> 104
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<220>
 <221> PEPTIDE
 <222> (1)..(104)
 <223> TFP3

<400> 5
 Met Gln Phe Lys Asn Val Ala Leu Ala Ala Ser Val Ala Ala Leu Ser
 1 5 10 15

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Ala Thr Ala Ser Ala Glu Gly Tyr Thr Pro Gly Glu Pro Trp Ser Thr
 20 25 30
 Leu Thr Pro Thr Gly Ser Ile Ser Cys Gly Ala Ala Glu Tyr Thr Thr
 35 40 45
 Thr Phe Gly Ile Ala Val Gln Ala Ile Thr Ser Ser Lys Ala Lys Arg
 50 55 60
 Asp Val Ile Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Thr Ser Ala
 65 70 75 80
 Ala Thr Ala Gln Ala Thr Asp Ser Gln Ala Gln Ala Thr Thr Thr Ala
 85 90 95
 Thr Pro Thr Ser Ser Glu Lys Ile
 100

<210> 6
 <211> 642
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> gene
 <222> (1)..(642)
 <223> TFP3

<400> 6
 gatcccgcc agcccttcca gcttttcttt ttcccttttt gctacggtcg agacacggtc 60
 gcccaaaaga aacgggtcag cgtgtactgc gccaaaaaaa ttgcgcccga ttttaagctaa 120
 acgtccacaa acaaaaacaa aaataagaaa taggttgaca gtgggtgaaa aattctcgaa 180
 gggttcatct ccaaacagtc agtatataag tattcgggaa agagagccaa tctatcttgt 240
 gggtgggtccta tcttaacctt ctctttttgg cagtagtaat tglaaatcaa gacacataaa 300
 actattttac tcgctaaact tacatctaaa atgcaattca aaaacgtcgc cctagctgcc 360
 tccgttgctg ctctatccgc cactgcttct gctgaagggt acactccagg tgaacctgg 420
 tccaccttaa cccaacagg ctccatctct tgtgggtgct cgaatacac taccaccttt 480
 ggatgtgctg ttcaagotat tacctcttca aaagctaaga gagacgttat ctctcaaatt 540
 ggtgacggtc aagtccaagc cacttctgct gctactgctc aagccaccga tagtcaagcc 600
 caagctacta ctaccgtac cccaaccagc tccgaaaaga tc 642

<210> 7
 <211> 50
 <212> PRT
 <213> *Hansenula polymorpha*

<220>
 <221> PEPTIDE
 <222> (1)..(50)
 <223> TFP4

<400> 7
 Met Arg Phe Ala Glu Phe Leu Val Val Phe Ala Thr Leu Gly Gly Gly
 1 5 10 15
 Met Ala Ala Pro Val Glu Ser Leu Ala Gly Thr Gln Arg Tyr Leu Val
 20 25 30
 Gln Met Lys Glu Arg Phe Thr Thr Glu Lys Leu Cys Ala Leu Asp Asp
 35 40 45
 Lys Ile
 50

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<210> 8
 <211> 179
 <212> DNA
 <213> Hansenula polymorpha

<220>
 <221> gene
 <222> (1)..(179)
 <223> TFP4

<400> 8
 gatccgcttt ttattgcttt gctttgctaa tgagatttgc agaattcttg gtgglatattg 60
 ccacgltagg cgggggggatg gctgcaccgg ttgagtctct ggccgggacc caacggtatc 120
 tggtgcaaat gaaggagcgg ttcaccacag agaagctgtg tgctttggac gacaagatc 179

<210> 9
 <211> 71
 <212> PRT
 <213> Saccharomyces cerevisiae

<220>
 <221> PEPTIDE
 <222> (1)..(71)
 <223> TFP1-3

<400> 9
 Met Phe Asn Arg Phe Asn Lys Phe Gln Ala Ala Val Ala Leu Ala Leu
 1 5 10 15
 Leu Ser Arg Gly Ala Leu Gly Asp Ser Tyr Thr Asn Ser Thr Ser Ser
 20 25 30
 Ala Asp Leu Ser Ser Ile Thr Ser Val Ser Ser Ala Ser Ala Ser Ala
 35 40 45
 Thr Ala Ser Asp Ser Leu Ser Ser Ser Asp Gly Thr Val Tyr Leu Pro
 50 55 60
 Ser Thr Thr Ile Ser Gly Asp
 65 70

<210> 10
 <211> 329
 <212> DNA
 <213> Saccharomyces cerevisiae

<220>
 <221> gene
 <222> (1)..(329)
 <223> TFP1-4

<400> 10
 ggatccatgt tcaatcggtt taacaaattc caagctgctg tcgctttggc cctactctct 60
 cgcggcgctc tcggtgactc ttacaccaat agcacctcct ccgcagactt gagttctatc 120
 acttcgctct cgtcagctag tgcaagtgcc accgcttccg actcactttc ttccagtgac 180
 gglaccgttt atttgccatc cacaacaatt agcggtgatc tcacagttac tggtaaagta 240
 attgaaccg aggcctgga agtcgctgcc ggtggttaagt tgactttact tgacggtgaa 300
 aaatacgtct tctcatctga tcctctaga 329

<210> 11
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
<223> JH97(Sfi-HSA-forward primer)

<400> 11
ccggccatta cggccgtgat gcacacaaga gtgag 35

<210> 12
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> JH119(Sfi-HSA-reverse primer)

<400> 12
ccggccgagg cggcctaagc ctaaggcag 29

<210> 13
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> JH99(Sfi-INV-forward primer)

<400> 13
gggcggccgc ctcggcccta gataaaaggc caatgacaaa cgaaactagc 50

<210> 14
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> JH100(SalI-INV-reverse primer)

<400> 14
ccgtcgactt actatittac ttcccttact tg 32

<210> 15
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> JH106(Sfi-IL2-forward primer)

<400> 15
gcggccatta cggccgtgca cctacttcaa gttctac 37

<210> 16
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> JH107(Sfi-IL2-reverse primer)

<400> 16
gcggccatta cggccgtgca cctacttcaa gttctac 37

<210> 17
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> JH120(BamHI-IL2-1-forward primer)

<400> 17
cgggatccgc acctacttica agttct 26

<210> 18
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> JH121(BamHI-IL2-2-forward primer)

<400> 18
cgggatcctg cacctacttc aagttct 27

<210> 19
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> JH122(BamHI-IL2-3-forward primer)

<400> 19
cgggatcctt gcacctactt caagttct 28

<210> 20
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> JH123(INV-1-reverse primer)

<400> 20
ccattgaagg aaccaacaaa at 22

<210> 21
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> JH124(INV-forward primer)

<400> 21
attttgttgg ttccttcaat gg 22

<210> 22
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> JH95(INV-2-reverse primer)

<400> 22
ggctcgagct attttacttc ccttacttg 29

<210> 23
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> JH132(SacI-GAL-forward primer)

<400> 23
gggagctcat cgcttcgctg att 23

<210> 24
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> JH137(IL-2-Term-reverse primer)

<400> 24
ccgtcgactt aagttagtgt tgagatg 27

<210> 25
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> HY22(TFP1-LDKR-reverse primer)

<400> 25
gaacttgaag taggtgccct tttatctaga ggatcagatg agaagac 47

<210> 26
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> HY23(TFP1-LDKR-forward primer)

<400> 26
tcttctcatc tgatcctcta gataaaaggg cacctacttc aagttc 46

<210> 27
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> HY20(TFP2-LDKR-reverse primer)

<400> 27
gaacttgaag taggtgccct tttatctaga ggatcgttca aactcc 46

<210> 28
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> HY21(TFP2-LDKR-forward primer)

<400> 28
ggagtttgaa cgatcctcta gataaaaggg cacctacttc aagttc 46

<210> 29
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> HY24(TFP4-LDKR-reverse primer)

<400> 29
gaacttgaag taggtgccct tttatcaagg atcttgcgt ccaaagc 47

<210> 30
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> HY25(TFP4-LDKR-forward primer)

<400> 30
gctttggaag acaagatcct tgataaaagg gcacctactt caagttc 47

<210> 31
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> JH143(XbaI-TFP1-d-reverse primer)

<400> 31
cctctagaat caccgctaatt tgttgtg 27

<210> 32
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> JH142(XbaI-TFP1-c-reverse primer)

<400> 32
cctctagaagg tgctatttgt gtaagag 27

<210> 33
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> JH141(XbaI-TFP1-b-reverse primer)

<400> 33
cctctagaac cgagagcgcc gcgagag 27

<210> 34
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> JH140(SpeI-XbaI-LDKR-forward primer)

<400> 34
ggactagtct agataaaagg gcacc 25

<210> 35
<211> 42
<212> DNA
<213> Artificial Sequence

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<220>

<223> HY38(TFP1-UTR-forward primer)

<400> 35

gaatttttga aaattcaagg atccaigtgc aatcgtttta ac

42

<210> 36

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> JH144(GCSF-forward primer)

<400> 36

cctctagata aaaggacccc cctgggccct gcc

33

<210> 37

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> JH145(GCSF-reverse primer)

<400> 37

ggcagctgga tgtattttac atggggag

28

<210> 38

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> HY17(TFP3-LDKR-reverse primer)

<400> 38

gaacttgaag taggtgccct tttatcaagg atcttttcgg agc

43

<210> 39

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> HY18(TFP3-LDKR-forward primer)

<400> 39

gctccgaaaa gatccttgat aaaagggcac ctacttcaag ttc

43

<210> 40

<211> 134

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> PEPTIDE

<222> (1)..(134)

<223> TFP3-1-1

<400> 40

Met Gln Phe Lys Asn Val Ala Leu Ala Ala Ser Val Ala Ala Leu Ser
1 5 10 15Ala Thr Ala Ser Ala Glu Gly Tyr Thr Pro Gly Glu Pro Trp Ser Thr
20 25 30

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Leu Thr Pro Thr Gly Ser Ile Ser Cys Gly Ala Ala Glu Tyr Thr Thr
 35 40 45
 Thr Phe Gly Ile Ala Val Gln Ala Ile Thr Ser Ser Lys Ala Lys Arg
 50 55 60
 Asp Val Ile Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Thr Ser Ala
 65 70 75 80
 Ala Thr Ala Gln Ala Thr Asp Ser Gln Ala Gln Ala Thr Thr Thr Ala
 85 90 95
 Thr Pro Thr Ser Ser Glu Lys Ile Ser Ser Ser Ala Ser Lys Thr Ser
 100 105 110
 Thr Asn Ala Thr Ser Ser Ser Cys Ala Thr Pro Ser Leu Lys Asp Ser
 115 120 125
 Ser Cys Lys Asn Ser Gly
 130

<210> 41
 <211> 402
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> gene
 <222> (1)..(402)
 <223> TFP3-1-1

<400> 41
 atgcaattca aaaacgtcgc cctagctgcc tccgttgctg ctctatccgc cactgcttct 60
 gctgaaggtt acactccagg tgaacctgg tccaccttaa cccaaccgg ctccatctct 120
 tgttggtctg ccgaatacac taccaccttt ggtattgctg ttcaagctat taccctttca 180
 aaagctaaga gagacgttat ctctcaaatt ggtgacggtc aagtccaagc cacttctgct 240
 gctactgctc aagccaccga tagtcaagcc caagctacta ctaccgctac cccaaccagg 300
 tccgaaaaga tctcttctc tgcattctaa acattctacta atgccacatc atcttctgt 360
 gccactccat ctitgaaaga tagctcatgt aagaattctg gt 402

<210> 42
 <211> 143
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<220>
 <221> PEPTIDE
 <222> (1)..(143)
 <223> TFP3-1-2

<400> 42
 Met Gln Phe Lys Asn Val Ala Leu Ala Ala Ser Val Ala Ala Leu Ser
 1 5 10 15
 Ala Thr Ala Ser Ala Glu Gly Tyr Thr Pro Gly Glu Pro Trp Ser Thr
 20 25 30
 Leu Thr Pro Thr Gly Ser Ile Ser Cys Gly Ala Ala Glu Tyr Thr Thr
 35 40 45
 Thr Phe Gly Ile Ala Val Gln Ala Ile Thr Ser Ser Lys Ala Lys Arg
 50 55 60
 Asp Val Ile Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Thr Ser Ala
 65 70 75 80
 Ala Thr Ala Gln Ala Thr Asp Ser Gln Ala Gln Ala Thr Thr Thr Ala

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85 90 95
 Thr Pro Thr Ser Ser Glu Lys Ile Ser Ser Ser Ala Ser Lys Thr Ser
 100 105 110
 Thr Asn Ala Thr Ser Ser Ser Cys Ala Thr Pro Ser Leu Lys Asp Ser
 115 120 125
 Ser Cys Lys Asn Ser Gly Thr Leu Glu Leu Thr Leu Lys Asp Gly
 130 135 140

<210> 43
 <211> 429
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> gene
 <222> (1)..(429)
 <223> TFP3-1-2

<400> 43
 atgcaattca aaaacgtcgc cctagctgcc tccgttgctg ctctatccgc cactgcttct 60
 gctgaagggt acactccagg tgaaccatgg tccaccttaa cccaaccgg ctccatctct 120
 tgttggtgctg ccgaatacac taccaccttt ggtattgctg ttcaagctat tacctcttca 180
 aaagctaaga gagacgttat ctctcaaatt ggtgacggtc aagtccaagc cacttctgct 240
 gctactgctc aagccaccga tagtcaagcc caagctacta ctaccgctac cccaaccagc 300
 tccgaaaaga tctcttctct tgcactctaa acatctacta atgccacatc atcttcttgt 360
 gccactccat ctttgaaaga tagtcatgt aagaattctg gtaccttaga atgaccttg 420
 aaggacggt 429

<210> 44
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> BglII-GAP-forward primer

<400> 44
 gcaagatctg gatccttttt tgtag 25

<210> 45
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> GAP-EcoRI-reverse primer

<400> 45
 aagaattctt gatagttgtt caattg 26